RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/798,096 A*
Source: *IFWO*
Date Processed by STIC: *7/27/04*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 4.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04): U S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/798,096 A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length

Sequence(s)___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing.

6 ___ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences

8 ___ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 ___ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species)   <220>.<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n/Xaa

"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

IFWO

RAW SEQUENCE LISTING   DATE: 07/27/2004
PATENT APPLICATION: US/10/798,096A   TIME: 11:56:44

          Input Set : A:\pto.lm.TXT
          Output Set: N:\CRF4\07272004\J798096A.raw

     3 <110> APPLICANT: Rea-Min Chu
     4   Ching-Yi Lin
     5   Ya-Wen Hsiao
     6   Kuang-Wen Liao
W--> 7 <120> TITLE OF INVENTION: COMPLEX IMMUNO-GENE MEDICAL COMPOSITION FOR INHIBITING TUMOR
CELLS
W--> 8 <130> FILE REFERENCE: P/741-176
W--> 9 <140> CURRENT APPLICATION NUMBER: 10/798,096A
    10 <141> CURRENT FILING DATE: 2004-03-11
W--> 11 <160> NUMBER OF SEQ ID: 4

(handwritten) Mandatory, please insert <220>, <221>, <222>, <223> whenever <223> is present.

ERRORED SEQUENCES

(handwritten) ✓ please see item # 1 on error summary sheet.

(handwritten) Does Not Comply Corrected Diskette Needed (pgs. 1-3)

    13 <210> SEQ ID NO: 1
    14 <211> LENGTH: 636
    15 <212> TYPE: DNA
    16 <213> ORGANISM: Human
    17 <223> OTHER INFORMATION: IL-6
W--> 19 <400> SEQUENCE: 1
E--> 21 atg aac tcc ttc tcc aca agc gcc ttc ggt cca gtt gcc tcc tcc ctg ggg ctg ctc ctg
    22 60
    23 Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser Leu Gly Leu Leu Leu
    24 1   5   10   15   20
E--> 26 gtg ctg cct gct gcc ttc cct gcc cca gta ccc cca gga gaa gat tcc aaa gat gta gcc
    27 120
    28 Val Leu Pro Ala Ala Phe Pro Ala Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val Ala
    29   25   30   35   40
E--> 31 gcc cca cac aga cag cca ctc acc tct tca gaa cga att gac aaa caa att cgg tac atc
    32 180
    33 Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile
    34   45   50   55   60
E--> 36 ctc gac ggc atc tca gcc ctg aga aag gag aca tgt aac aag agt aac atg tgt gaa
    37 agc 240
    38 Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser
    39   65   70   75   80
E--> 41 agc aaa gag gca ctg gca gaa aac aac ctg aac ctt cca aag atg gct gaa aaa gat gga
    42 300
    43 Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp
W--> 44 Gly
W--> 45   85   90   95   100
E--> 47 tgc ttc caa tct gga ttc aat gag gag act tgc ctg gtg aaa atc atc act ggt ctt ttg
    48 360
    49 Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu Leu

(handwritten right margin) ← only 16 codons are valid per line

RAW SEQUENCE LISTING   DATE: 07/27/2004
PATENT APPLICATION: US/10/798,096A   TIME: 11:56:44

Input Set : A:\pto.lm.TXT
Output Set: N:\CRF4\07272004\J798096A.raw

```
W--> 50              105             110             115             120
E--> 52 gag ttt gag gta tac cta cag tac ctc cag aac aga ttt gag agt agt gag gaa caa gcc
     53 (420)
     54 Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala
W--> 55    125              130             135    140
E--> 57 aga gct gtg cag atg agt aca aaa gtc ctg atc cag ttc ctg cag aaa aag gca aag aat
     58 (480)
     59 Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn
W--> 60              145             150             155             160
E--> 62 cta gat gca ata acc acc cct gac cca acc aca aat gcc agc ctg ctg acg aag ctg cag
     63 (540)
     64 Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln
W--> 65              165             170             175             180
E--> 67 gca cag aac cag tgg ctg cag gac atg aca act cat ctc att ctg cgc agc ttt aag gag
     68 (600)
     69 Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu
W--> 70              185             190             195             200
E--> 72 ttc gtg cag tcc agc ctg agg gct ctt cgg caa atg
     73 (636)
     74 Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met
W--> 75              205             210
     77 <210> SEQ ID NO: 2
     78 <211> LENGTH: 60
     79 <212> TYPE: DNA
     80 <213> ORGANISM: Human
     81 <223> OTHER INFORMATION: IL-2 Signal Peptide
E--> 83 <400> SEQUENCE: 2
E--> 85 atg tac agg atg caa ctc ctg tct tgc att gca cta agt ctt gca ctt gtc aca aac agt
     86 (60)
     87 Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser
     88 1            5            10            15            20
     91 <210> SEQ ID NO: 3
     92 <211> LENGTH: 342
     93 <212> TYPE: DNA
     94 <213> ORGANISM: Human
     95 <223> OTHER INFORMATION: Partial Sequence Encoding Human IL-15
     97 <400> SEQUENCE: 3
E--> 99 aac tgg gtg aat gta ata agt gat ttg aaa aaa att gaa gat ctt att caa tct atg cat
     100 (60)
     101 Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
     102 1            5            10            15            20
E--> 104 att gat gct act tta tat acg gaa agt gat gtt cac ccc agt tgc aaa gta aca gca atg
     105 (120)
     106 Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met
     107 1            25            30            35            40
E--> 109 aag tgc ttt ctc ttg gag tta caa gtt att tca ctt gag tcc gga gat gca agt att cat
     110 (180)
     111 Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His
     112 1            45            50            55            60
```

(handwritten annotations): please insert <220> whenever <221>, <222> or <223> is present. // same error

(handwritten annotations): insert <220> // same error

(handwritten annotations): only 16 codons valid per line.

(handwritten annotations): error on this sheet

```
B--> 114  gat aca gta gaa aat ctg atc atc cta gca aac aac agt ttg tct tct aat ggg aat gta
     115  240
     116  Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn
W--> 117  Val
W--> 118              65              70              75              80
B--> 120  aca gaa tct gga tgc aaa gaa tgt gag gaa ctg gag gaa aaa aat att aaa gaa ttt ttg
     121  300
     122  Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
W--> 123              85              90              95              100
B--> 125  cag agt ttt gta cat att gtc caa atg ttc atc aac act tct
     126  342
     127  Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
W--> 128              105             110
     131  <210> SEQ ID NO: 4
     132  <211> LENGTH: 402
     133  <212> TYPE: DNA
     134  <213> ORGANISM: Artificial Sequence
W--> 135  <220> FEATURE: Bases 1-60 Code for IL-2 Signal Peptide
W--> 135  <220> FEATURE: Bases 1-60 Code for IL-2 Signal Peptide
     136  <223> OTHER INFORMATION: Artificial Chimeric Sequence Encoding IL-2SP/IL-15MP
     138  <400> SEQUENCE: 4
B--> 140  atg tac agg atg caa ctc ctg tct tgc att gca cta agt ctt gca ctt gtc aca aac agt
     141  60
     142  Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser
     143  1           5               10              15              20
B--> 145  aac tgg gtg aat gta ata agt gat ttg aaa aaa att gaa gat ctt att caa tct atg cat
     146  120
     147  Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
     148              25              30              35              40
B--> 150  att gat gct act tta tat acg gaa agt gat gtt cac ccc agt tgc aaa gta aca gca atg
     151  180
     152  Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met
     153              45              50              55              60
B--> 155  aag tgc ttt ctc ttg gag tta caa gtt att tca ctt gag tcc gga gat gca agt att cat
     156  240
     157  Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His
     158              65              70              75              80
B--> 160  gat aca gta gaa aat ctg atc atc cta gca aac aac agt ttg tct tct aat ggg aat gta
     161  300
     162  Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
     163              85              90              95              100
B--> 165  aca gaa tct gga tgc aaa gaa tgt gag gaa ctg gag gaa aaa aat att aaa gaa ttt ttg
     166  360
     167  Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
     168              105             110             115             120
B--> 170  cag agt ttt gta cat att gtc caa atg ttc atc aac act tct
     171  402
     172  Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
     173              125             130
```

[handwritten annotations: "delete", "← SAME error please do not insert a response beside", "Numeric identifier <220>"]

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/27/2004
PATENT APPLICATION: US/10/798,096A   TIME: 11:56:45

Input Set : A:\pto.lm.TXT
Output Set: N:\CRF4\07272004\J798096A.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 21,23,26,28,31,33,38,64,72
Seq#:2; Line(s) 87
Seq#:3; Line(s) 101,106,111,122,125
Seq#:4; Line(s) 142,147,152,157,162,167

VERIFICATION SUMMARY   DATE: 07/27/2004
PATENT APPLICATION: US/10/798,096A   TIME: 11:56:45 ·

Input Set : A:\pto.lm.TXT
Output Set: N:\CRF4\07272004\J798096A.raw

```
L:7 M:283 W: Missing Blank Line separator, <120> field identifier
L:8 M:283 W: Missing Blank Line separator, <130> field identifier
L:9 M:283 W: Missing Blank Line separator, <140> field identifier
L:11 M:283 W: Missing Blank Line separator, <160> field identifier
L:19 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:1
L:21 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:1
L:26 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:120 SEQ:1
L:31 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:180 SEQ:1
L:36 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:237 SEQ:1
L:41 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:300 SEQ:1
L:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:45 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:47 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:360 SEQ:1
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:52 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:420 SEQ:1
L:55 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:57 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:480 SEQ:1
L:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:62 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:540 SEQ:1
L:65 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:67 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:600 SEQ:1
L:70 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:72 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:636 SEQ:1
L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:83 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:2
L:85 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:2
L:97 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:3
L:99 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:3
L:104 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:120 SEQ:3
L:109 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:180 SEQ:3
L:114 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:240 SEQ:3
L:117 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:120 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:300 SEQ:3
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:125 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:342 SEQ:3
L:128 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:135 M:283 W: Missing Blank Line separator, <220> field identifier
L:135 M:256 W: Invalid Numeric/Header Field, <220> has non-blank data
L:140 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:4
L:145 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:120 SEQ:4
L:150 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:180 SEQ:4
L:155 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:240 SEQ:4
L:160 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:300 SEQ:4
L:165 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:360 SEQ:4
L:170 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:402 SEQ:4
```